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tga						3183

FIG.1

MGKTVVGASRMFWLMEFVPLLLALCPSEPAHALAPGSSRVLEFK
 ROSSKVPFEKGGKVTERVHFRPALVNVDGVMVALADARYETSDNLSLIDTVAKYS
 VDDGETWETQIAIKNSRASSVSRVVDPTVIVKGNKLYVLVGSYNSSRSYWTSHGDARD
 WDIILAUGEVTKSTAGGKITASIKWGPVSLKEFFPAEMEGMHTNQFLGGAGVALIVAS
 NGNLVYPVQVTNKKQVFSKIFYSEDEGKTWKFGEGRSDFGCSEPVALLEWEGKLIINT
 RVDYRRRLVYESSDMGNSWVEAVGTLRVWGPSPKSNQPGSQSSFTAVTIEGMRVMLF
 THPIINFKRWLRDRINLWLTDNQRIYNVGQVSI GDENSAYSSVLYKDDKLYCLHEINS
 NEVYSLVFARLVGELRIIKSVLQSWKNWDSHLSSICTPADPAASSSERGCCGPAVTTVG
 LVGFLSHSATKTEWEDAYRCVNASTANAERVPNGLKFAVGGGALWPVSQQGONQRYH
 FANHAFTLVASVTIHEVPSVASPLLGASLDSSGGKKLLGLSYDEKHQWQPIYGSTPVT
 PTGSWEMGKRYHVVLTMANKIGSVYIDGEPLEGSGQTVVPDGRTPDISHFYVGGYGRS
 DMPTISHVTNNVLLYNRQLNAEIRTLFLSQDLIGTEAHMGSSGSSAHSTPSTPAD
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 TPGDSSAHSTPSTPADNGAHSTPSAPADSNHAHSTPSTPGDNGAHSTPSAPADSNHAHST
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 AHSTPSIPGDSSAHSTPSAPADSSAHSTPSAPGDNGAHSTPSTPADNGANGTVLILHD
 GAAFSAFSGGGLLCAGALLLHVFMVAVEF

FIG.2

FIG. 3

605050" 6055550

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MLAPGSSRVELFKRQSSKVPFEKDGKVTERRVHSEFRLPALVNVD
GVMVALADARYETSDNDSLIDTVAKYSVDDGETWETQIAIKNSRASSVSRVVDPTVTV
KGNKLYVLVGSYNSSRSYWTSHGDARDWDILLAVGEVTKSTAGGKTASIKWGSFVSL
KEFFPAEMEGMHTNQFLGGAGVALVASNCNLVYPVQVTNKKQVFESKIFYSEDEGKTW
KFGKGRSAFGCSEPVALEWEGKLIINTRVDYRRRLVYESSDMGNSWLEAVGTLSRVWG
PSPKSNQPGSQSSFTAVTIEGMRVMLETHPLNFKGRWLRDRINLWLTDNQRIYNVGQV
SIGDENSAYSSVLYKDDKLYCLHEINSNEVYSLVFARLVGELRIKSVLQSWKNWDSH
LSSICTPADPPAASSSERGCCPAVTTVGLVGFLSHSAATKTEWEDAYRCVNASTANAERV
PNGLKFAGVGGGALWPPVSQQGQNQRYPFANHAFTTVASVTIHEVPSVASPLIGASLDS
SGGKLLGLSYDEREQWQPIYGSTPVTPTGSWEMGKRYHVVLTMANKIGSEYIDGEP
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QDLIGTEAHMDSSSDTSA

FIG.4



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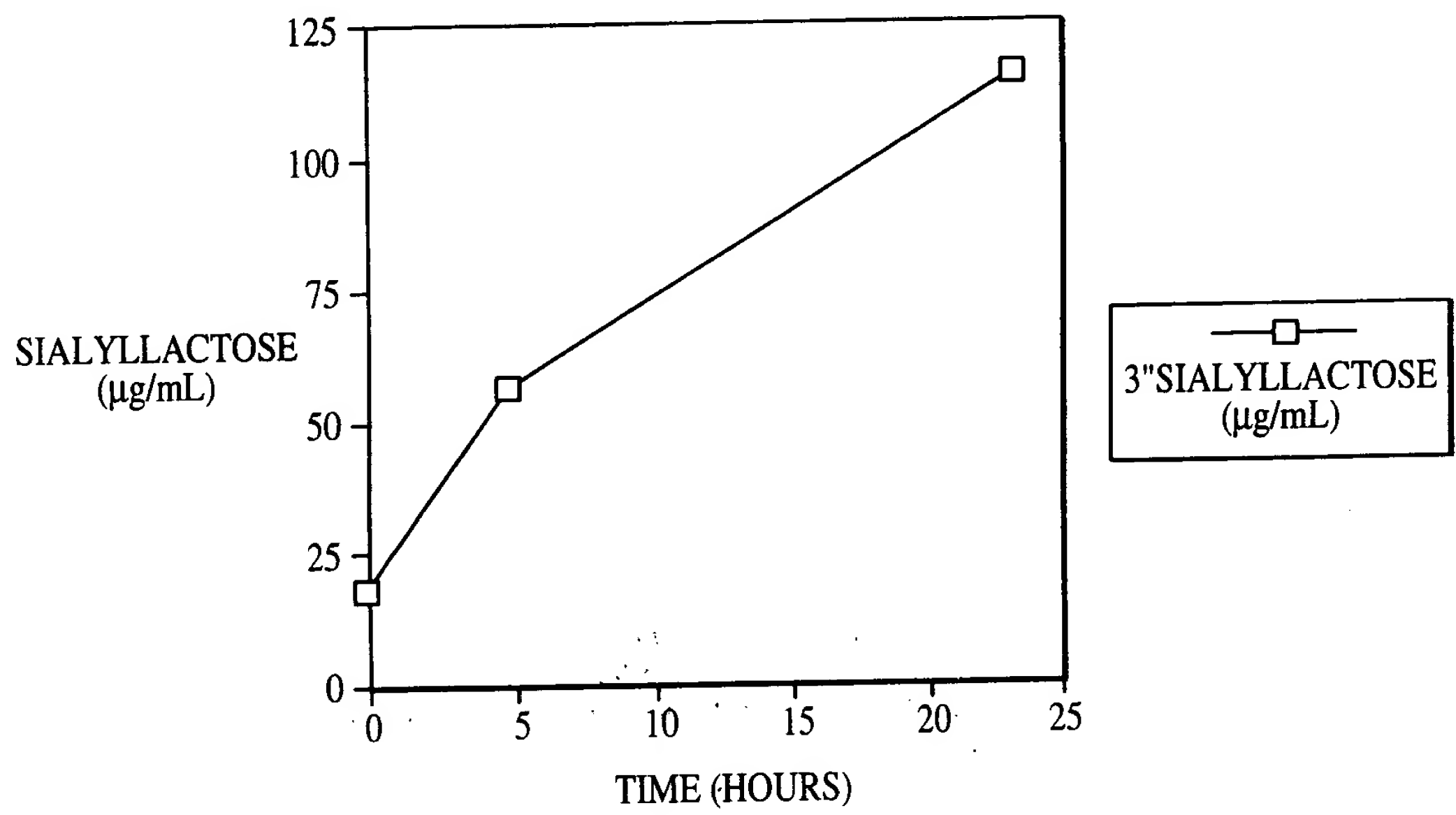


FIG.6

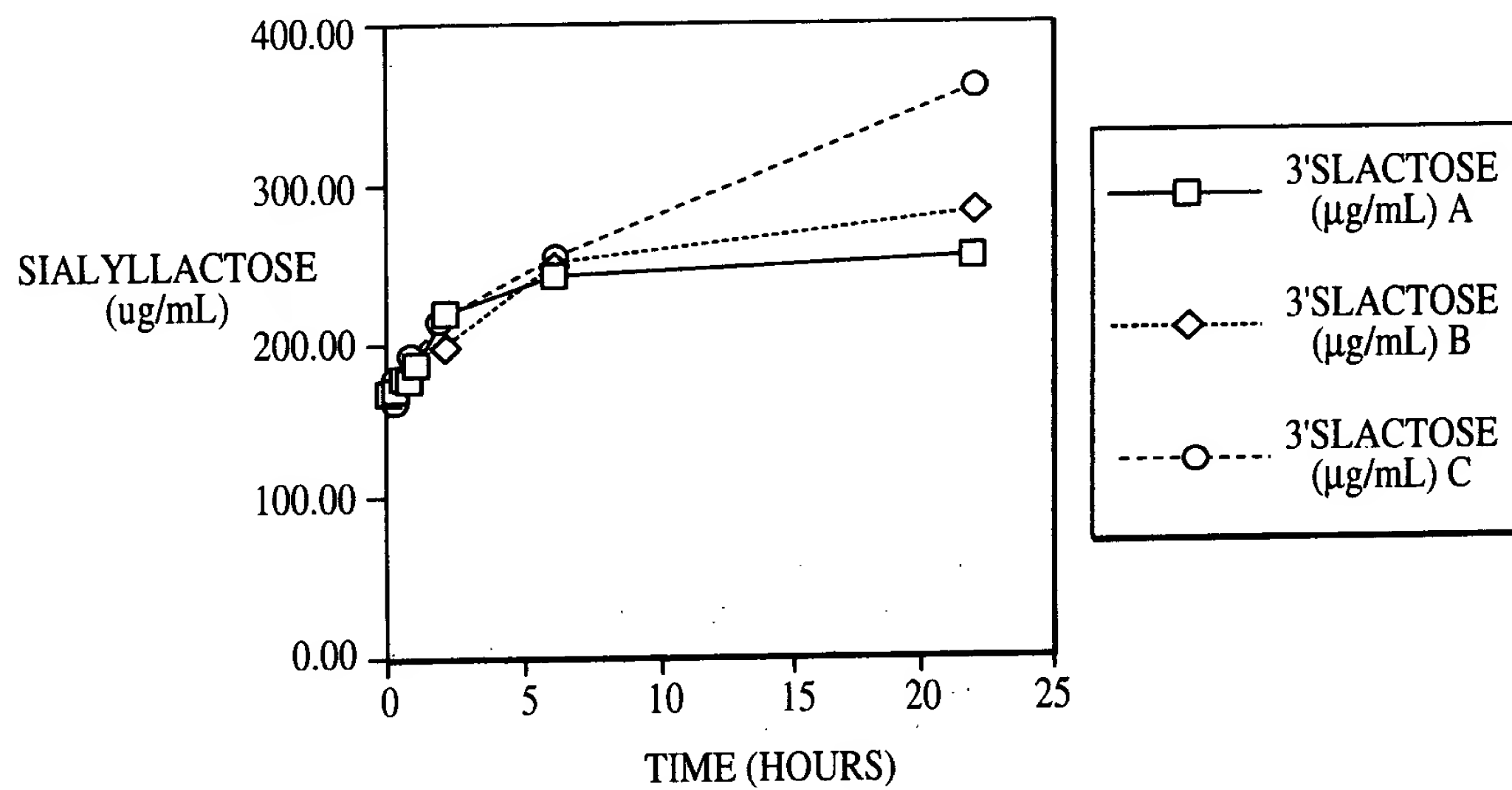


FIG.7A

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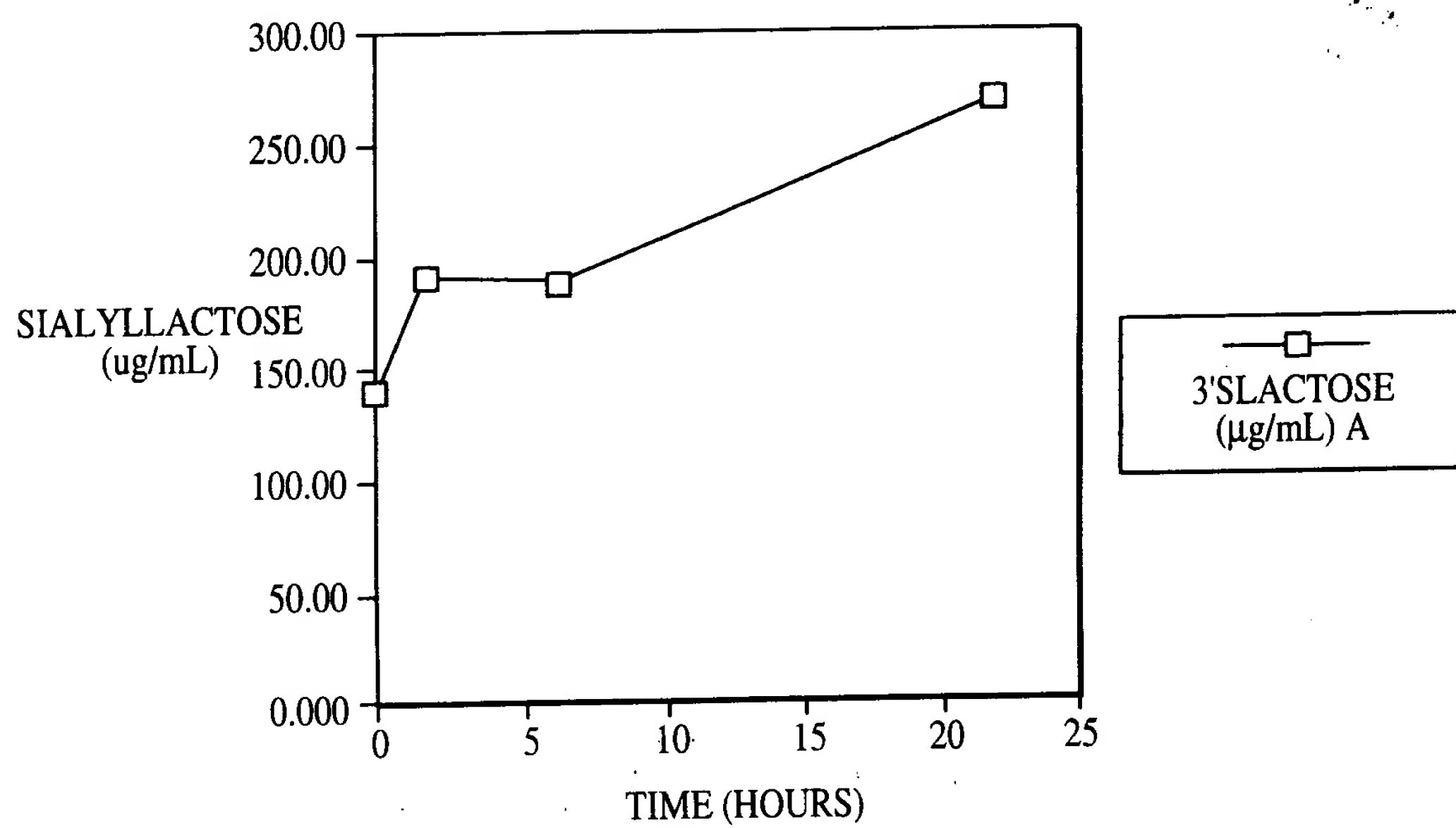


FIG.7B

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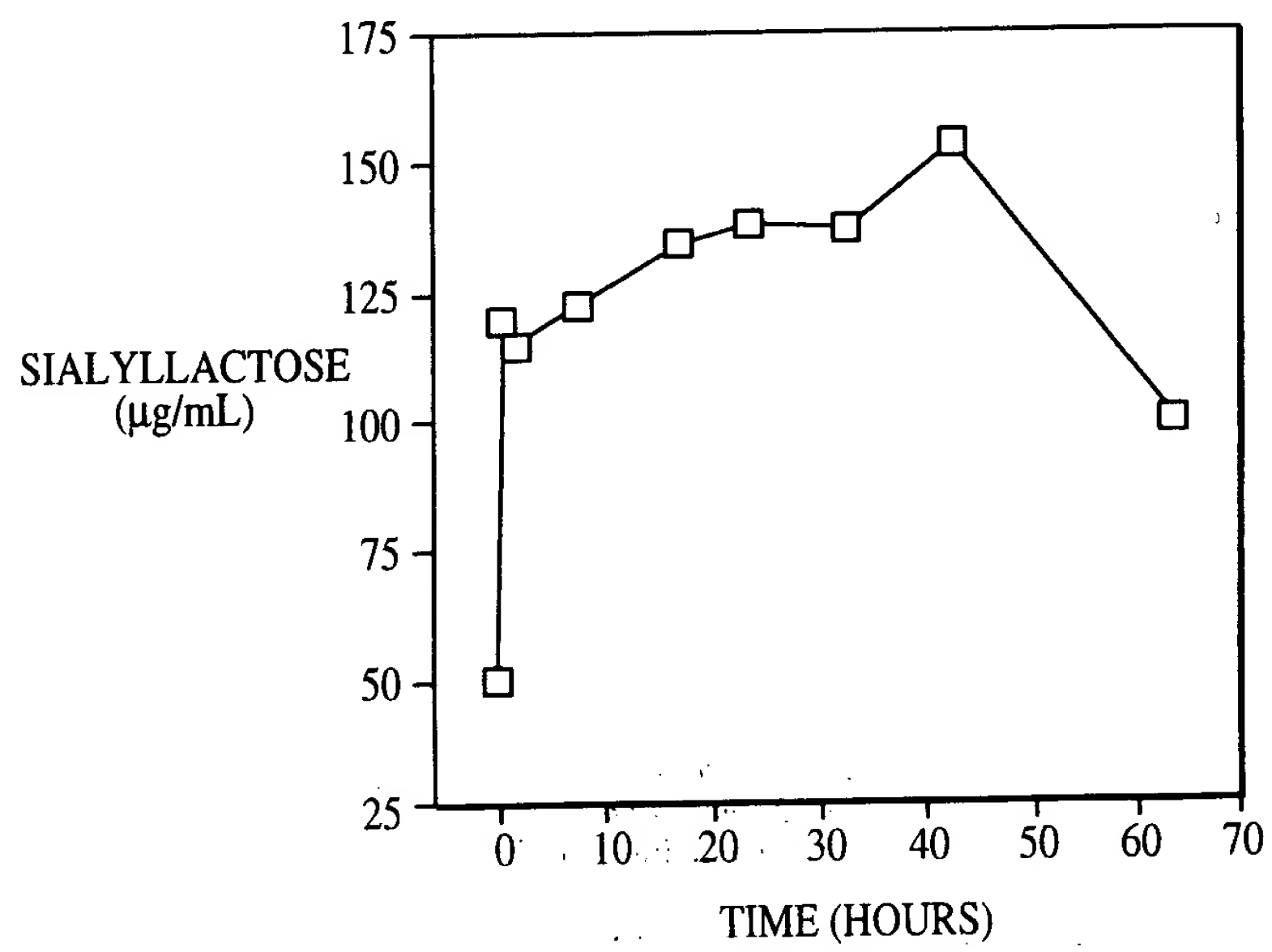


FIG.8

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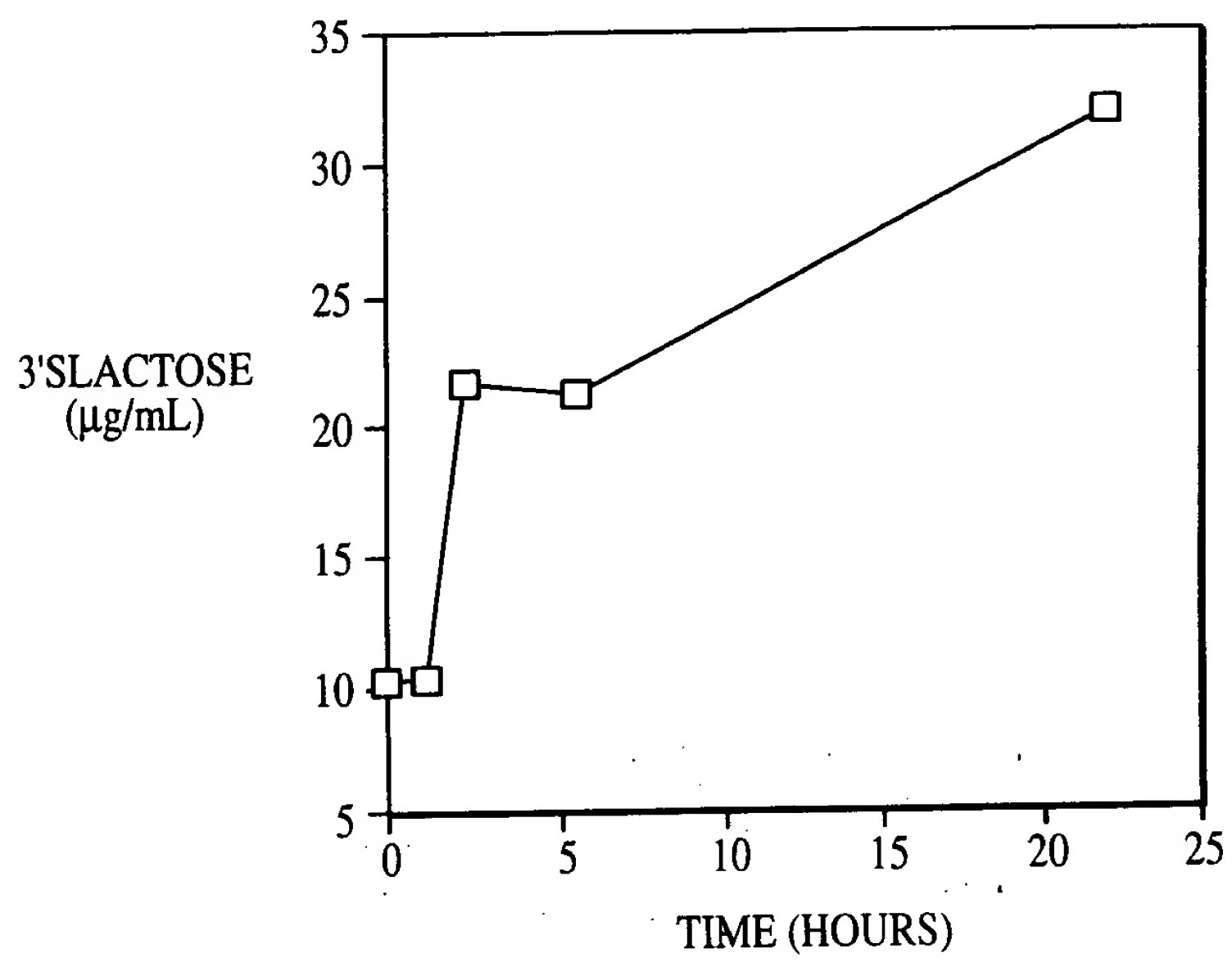


FIG.9